GENETIC ANALYSIS OF RABBIT LITTER TRAITS AT BIRTH AND WEANING

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ABSTRACT

Data on 260 litters were used to provide estimates of heritability, repeatability, genetic and phenotypic correlations for litter traits at birth and at weaning. Breed, sire within breed and doe within sire effects were found to be significant, (P<0.05) for litter size at birth and at weaning and for litter weight at birth and at weaning. Heritability estimates of 0.33±0.08, 0.38±0.02, 0.03±0.02 and 0.16 ± 0.05 were obtained for litter birth weight, litter size at birth, litter size at weaning and litter weaning weight, respectively. Repeatability estimates were found to be generally moderate to high. Genetic and phenotypic correlations were positive and significant (P<0.01). Selection for litter size at birth and litter birth weight are likely to result in improved litter size at weaning and litter weaning weight respectively.
Key words: Rabbit, litter size and weight, heritability, repeatability.

INTRODUCTION

The two-main tools for genetic improvement are selection and mating systems. To employ these tools, however, certain genetic parameters - heritability, repeatability and genetic correlations, must be determined. The knowledge of the genetic parameters enables the breeder to decide on the best method of selection to achieve rapid genetic progress. Such genetic studies for domestic rabbits are non-existent in Nigeria. However, reported estimates of heritability for litter size at birth were mostly below 0.20 (Garcia *et al*, 1980; Lukefahr, 1982; Khalil *et al*., 1987). Estimates of repeatability for litter traits were relatively low (Khalil *et al*., 1988; Rouvier *et al*., 1973).

The objectives of the present study were therefore to estimate the heritability and repeatability of rabbit litter traits and to determine both the phenotypic and genetic correlation's among them.

MATERIALS AND METHODS

Data on 260 litters comprising 24 Chinchilla (CH), 51 California (CL) 147 New Zealand White, 7 Chinchilla x New Zealand White (Ch-NZW), 17 New Zealand White x Chinchilla (NZW-CH) and 14 New Zealand White x New Zealand White x Chinchilla (NZW-NZW-CH) breeds of rabbits were used for this study. The data were collected at the Rabbitry Unit, Obafemi Awolowo University Teaching and Research Farm, Ile-Ife, Nigeria over a three year period (1988-1991). All the rabbits were housed in cages and fed *ad libitum* with pelleted rations containing 16.5% crude protein and 2884 Kcal GE/kg gross energy. *Panicum maximum* was also fed as supplementary ration. Vitalyte (composite minerals and vitamin supplement) was given in the drinking water to all pregnant does and their kids.

Matings were carried out in the morning and 14 days *post partum*. The does were palpated to determine pregnancy. Non-pregnant does were put up for mating again unitl conception occured. The litters were examined at birth for defects. The litter size size and litter weight at birth were recorded within 24 hours. A total of 76 does were mated to 34 bucks. In-breeding was avoided in the herd.

Data collected were litter size at birth and at weaning and litter weight at birth and at weaning (35 days).

Statistical Analysis

The data were subjected to analysis of variance for unequal subclass numbers using the model

$Y_{ijkl} = u+B_i + S_{ij} + D_{ijk} + e_{ijkl}$

where Y_{ijkl} = Observation on the lth litter belonging to the kth doe mated to the jth sire of ith breed.

u = Overall mean

B_i = effect of the ith breed

S^{ij} = effect of the jth sire of the ith breed

D_{ijk} = effect of the kth doe mated to the jth sire of ith breed

e_{ijkl}= random error.

Estimates of variance components were calculted using method 3 of Henderson (1953). By equating the mean square of each random effect to its expectation, variance component estimates of buck within breed (σ^2B), doe within buck within breed (σ^2D) and error (σ^2E) were obtained. These estimates were used to compute heritabilities, repeatabilities, genetic and phenotypic correlations.
Heritability estimates were obtained as:

$$h^2s = \frac{4\sigma^2B}{\sigma^2B + \sigma^2D + \sigma^2E}$$

while repeatability estimates were computed as

$$r = \frac{\sigma^2B + \sigma^2D}{\sigma^2D + \sigma^2D + \sigma^2E}$$

Standard errors for heritability and repeatability estimates were calculated using the formula described by Swiger *et al.* (1964). Estimates of genetic and phenotypic correlations were obtained by the LSMLIMW and MIXMDL programme of Harvey (1990).

RESULTS

The means squares of analysis of variance for the four traits are as shown in Table 1. Breed, sire within breed and doe within sire effects for all the traits considered were significant (P0.05). Table 2 shows the least squares means for all the traits for all breeds.

The CL breed had the least performance for all the traits considered except litter birth weight. All the other breds with the exception of CH-NZW were not significantly (P>0.05) different for all the traits. The CH-NZW kids had the best performance for all the traits except litter size at weaning. Mating of NZW-CH sires to NZW does did not improve the performance beyond that for the NZW breed.

The heritability estimates were low for weaning characteristics while it was moderate for birth traits. The repeatability estimates were, however, moderate to high for all the traits considered (Table 3).

Genetic and phenotypic correlation among the four traits were found to be generally positive and significant (P<0.05) (Table 4).

DISCUSSION

The breed differences for all the traits were not clear cut except for CL and CH-NZW breeds. However, CH-NZW breed recorded higher litter size at birth and litter weaning weight than all other breeds. This is similar to the observation of Somade and Adesina (1990) who attributed the higher performance to heretosis and recommended the use of NZW-CL does as dams and CH bucks as sires for raising 3 breed crosses. No doubt, crossbreeding would lead to improvement in litter traits. However, since the scope of the matings were limited it may not be appropriate yet to recommend a particular breeding scheme for use in the humid tropics of Nigeria.

Contrary to the reports of Rouvier *et al.* (1973), Patridge *et al.* (1981) and Khalil *et al.* (1988) significant buck effects were observed for all the traits. However, the maternal effects which had been reported by several workers to be significant for the weaning traits were also found to be significant for all the traits. The significant buck effect may be due to genotype-buck interaction.

Moderate heritability estimates obtained for birth-related characteristics indicate moderate genetic influence. Thus selection for the two

TABLE 1: MEAN SQUARES OF ANALYSIS OF VARIANCE ON LITTER WEIGHTS AND LITTER SIZES AT BIRTH AND AT WEANING.

Source of Variation		Litter birth weight			Litter size at birth			Litter weaning weight			Litter size at weaning	
	df	ms	Variance Component	df	ms	Variance Component	df	ms	Variance Component	df	ms	Variance Component
Breed	5	11543.21*		5	15.96*		5	158764.31*		5	9.74	
Sire within breed	28	12024.61**	526.31	28	25.41**	0.98	25	182421.29**	894.50	25	15.21*	0.28
Doe within	42	8003.57**	911.96	42	17.95**	3.60	38	176073.24**	28252.11	38	14.26**	3.00
Error	184	4883.70	4883.70	184	5.64	5.64	151	78956.61	78956.61	151	3.94	3.94

*P<0.05 **P<0.01

TABLE 2: LEAST SQUARES MEANS AND STANDARD ERRORS OF LITTER WEIGHTS AND LITTER SIZES AT BIRTH AND WEANING

	Litter birth weight (g)	Litter size at birth	Litter weaning weight (g)	Litter size at weaning
BREED[3]:				
CH	245.73 ± 16.40^{bc} (24)	5.38 ± 0.40^{bc} (24)	1608.01 ± 125^{b} (15)	3.89±0.19ab (15)
NZW	241.51 ± 17.90^{bc} (147)	5.49 ± 0.24^{b} (147)	1630.64 ± 102^{b} (135)	3.95 ± 0.26^{ab} (135)
CL	237.70 ± 19.30^{a} (51)	4.78 ± 0.10^{d} (51)	1394.15 ± 95^{c} (44)	$3.46\pm0.19_{c}$ (44)
CH-NZW	283.07 ± 19.30^{a} (7)	6.57 ± 0.24^{a} (7)	1840.64 ± 118^{a} (4)	4.14 ± 0.16^{a} (4)
NZW-CH	268.12 ± 16.90^{ab} (12)	5.59 ± 0.14^{b} (12)	1696.34 ± 114^{b} (10)	3.86 ± 0.23^{ab} (10)
NZW-NZW-CH	242.47 ± 15.70^{bc} (14)	5.00 ± 0.19^{cd} (14)	1665.21 ± 134^{b} (12)	3.81 ± 0.26^{ab} (12)

[1]Figures in parentheses are number of observations
[2]Means within columns with different superscripts are significantly different ($P<0.05$)
[3]CH = Chinchilla
NZW = New Zealand white
CL = California white
CH-NZW = Chinchilla x New Zealand white
NZW-CH = New Zealand white x Chinchilla
NZW-NZW = New Zealand white x (New Zealand white x Chinchilla)

TABLE 3: HERITABILITY AND REPEATABILITY ESTIMATES WITH STANDARD ERROR FOR THE LITTER TRAITS

	h^2	r
Litter birth weight	0.33±0.08	0.23±0.10
Litter size at birth	0.38±0.02	0.45±0.12
Litter size at weaning	0.03±0.02	0.27±0.15
Litter weaning weight	0.16±0.05	0.45±0.07

TABLE 4: PHENOTYPIC AND GENETIC CORRELATIONS[a] AMONG LITTER TRAITS IN DOMESTIC RABBITS

	X_1	X_2	X_3	X_4
Litter size at birth (X_1)		0.89**	0.67**	0.63**
Litter birth weight (X_2)	0.67**			0.81**
Litter size at weaning (X_3)	0 54**			
Litter weaning weight (X_4)	0.52**	0.52**	0.94**	0.91**

[a]The phenotypic correlations are above the diagonal line while the genetic correlations are below.

**P<0.01)

traits - litter size and litter weight at birth should result in genetic improvement of the traits. Litter size and litter weight at weaning had low heritability. This is an indication of low genetic attribute but high environmental influence. Owen (1976) had observed that high ambient temperatures of the tropical environment led to some depression in reproductive and growth performance. Thus, management practices that minimize the effect of the high ambient temperature on the rabbits will result in improved performance.

Khalil *et al.* (1988) reported that maternal effects resulted in the high heritability estimates obtained for pre-weaning traits. This observation is true for this study. Rouvier *et al.* (1973), and Khalil and Afifi (1986) thus indicated that pre-weaning litter traits are female traits and could be improved through the selection of a doe based on her own or her dam's performance and well as through selected of sires during progeny testing.

The moderate to high repeatability estimates show that great reliability can be put on selection or culling of does and sires based on 1 or 2 records. Thus leading to improvement in the productivity of the herd.

The high genetic and phenotypic correlations obtained are consistent with the reports of Afifi *et al.* (1980), Garcia *et al.*(1988). Selection for litter size and litter weight at birth will thus lead to improvement in litter size and litter weight at weaning, as earlier suggested by Odubote and Akinokun (1991).

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